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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/601,777	06/24/2003	Tadashi Okamoto	03560.003310.	9502
5514	7590	11/04/2005	EXAMINER	
FITZPATRICK CELLA HARPER & SCINTO 30 ROCKEFELLER PLAZA NEW YORK, NY 10112			DEJONG, ERIC S	
			ART UNIT	PAPER NUMBER
			1631	

DATE MAILED: 11/04/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

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APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
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EXAMINER
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ART UNIT	PAPER
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20051101

DATE MAILED:

**Please find below and/or attached an Office communication concerning this application or proceeding.**

Commissioner for Patents

See attached Office Communication regardsing the response filed by applicants on 08/24/2005.

## OFFICE COMMUNICATION

The reply filed on 24 August 2005 is not fully responsive to the prior Office Action because of the following omission(s) or matter(s):

The previous Office action on pages 2 and 3, bridging paragraph stated

"This application contains sequence disclosures that are encompassed by the definitions for nucleotide and /or amino acid sequences set forth in CFR § 1.821(a)(1) and (a)(2). See, for example, page 31, lines 7 and 8, page 35, lines 20 and 21, page 36, line 19, page 37, lines 23 and 24, and page 41, line 10. However, this application fails to comply with the requirements of CFR § 1.821 through 1.825 because it lacks any submission of a computer readable form sequence listing, a paper copy for the specification, a statement under CFR § 1.821(f) and (g), and SEQ ID numbers cited along with each sequence in the specification or Figures. Applicants are also reminded that SEQ ID numbers are not required in the Figures per se, however, the corresponding SEQ ID numbers then are required in the Brief Description of the Drawings section in the specification. Applicants are also reminded that a CD\_ROM sequence listing submission may replace the paper and computer readable form sequence listing copies. Applicants are given the same response time regarding this failure to comply as that set forth to respond to this office action. Failure to respond to this requirement may result in abandonment of the instant application or a notice of a failure to fully respond to this Office Action."

Applicants response is not completely responsive to the above requirement as the instant specification it fails to comply with the requirements of CFR § 1.821 through 1.825 because it lacks any submission of SEQ ID numbers cited along with each sequence in the specification. The substitute specification filed by applicants on 24 August 2005 does not include the use of the sequence identifier "SEQ ID NO:" for sequences now disclosed on page 29, lines 4 and 5, page 33, lines 13 and 14, page 34, line 10, page 35, lines 16 and 17, and page 39, line 11.

Art Unit: 1631

MPEP §2421.02 (d) states:

“Where the description or claims of a patent application discuss a sequence that is set forth in the “Sequence Listing” in accordance with paragraph (c) of this section, reference must be made to the sequence by use of the sequence identifier, preceded by “SEQ ID NO:” in the text of the description or claims, even if the sequence is also embedded in the text of the description or claims of the patent application.”

It is acknowledged that the specification identifies sequences as “Sequence No. 1” (page 29, line 3), “Sequence No. 2” (page 33, line 12), “Sequence No. 3” (page 34, line 9), “Sequence No. 2’ ” (page 35, line 15), and Sequence No. 4” (page 39, line 10). For clarification purposes, Applicants should replace the existing sequence identifiers with “SEQ ID NO:” followed by the appropriate number so that the submitted sequence listing and sequence identifiers recited in the specification are identical.

Further, included is a copy of the Raw Sequence Listing Error Report generated on 08/29/2005. For clarity of the record, said Error Report is considered to be part of the basis warranting the instant Notice of Non-Compliance.

See 37 CFR 1.111. Since the above-mentioned reply appears to be *bona fide*, applicant is given **ONE (1) MONTH or THIRTY (30) DAYS** from the mailing date of this notice, whichever is longer, within which to supply the omission or correction in order to avoid abandonment. **EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).**

### ***Conclusion***

Any inquiry of a general nature or relating to the status of this application should be directed to Legal Instrument Examiner, Tina Plunkett, whose telephone number is (571) 272-0549.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Eric S. DeJong whose telephone number is (571) 272-6099. The examiner can normally be reached on 8:30AM-5:00PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ardin Marschel, Ph.D. can be reached on (571) 272-0718. The fax phone number for the organization where this application or proceeding is assigned is (571) 273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight

Art Unit: 1631

(EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

For all other customer support, please call the USPTO Call Center at (800) 786-9199.

EDJ

*EDJ*

*John S. Brusca 1 November 2005*

**JOHN S. BRUSCA, PH.D  
PRIMARY EXAMINER**

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/601,777  
Source: IFw/6  
Date Processed by STIC: 8/29/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/601,777

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length     Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
                    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    This sequence is intentionally skipped  
  
                    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
                    <210> sequence id number  
                    <400> sequence id number  
                    000
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>     Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
                    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa     "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid





IFW16

## RAW SEQUENCE LISTING

DATE: 08/29/2005

PATENT APPLICATION: US/10/601,777

TIME: 17:20:57

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\08292005\J601777.raw

*see item 4 on Euro  
summary  
sheet*

2 <110> APPLICANT: Okamoto, Tadashi  
3 Takase, Hiromitsu  
4 Hashimoto, Hiroyuki  
W--> 5 <120> TITLE OF INVENTION: A METHOD FOR ACQUIRING INFORMATION OF A BIOCHIP USING TIME OF FLIGHT  
W--> 6 SECONDARY  
W--> 7 ION MASS SPECTROMETRY AND AN APPARATUS FOR ACQUIRING INFORMATION FOR THE  
W--> 8 APPLICATION  
W--> 9 THEREOF  
W--> 10 <130> FILE REFERENCE: 03560.003310  
W--> 11 <140> CURRENT APPLICATION NUMBER: US/10/601,777  
12 <141> CURRENT FILING DATE: 2003-06-24  
13 <150> PRIOR APPLICATION NUMBER: JP 2002-191208  
14 <151> PRIOR FILING DATE: 2002-06-28  
15 <150> PRIOR APPLICATION NUMBER: JP 2003-161862  
16 <151> PRIOR FILING DATE: 2003-06-06  
W--> 17 <160> NUMBER OF SEQ ID: 5

*Does Not Comply  
Corrected Diskette Needed*

## ERRORED SEQUENCES

42 <210> SEQ ID NO: 4  
43 <211> LENGTH: 18  
44 <212> TYPE: DNA  
45 <213> ORGANISM: Artificial sequence  
W--> 46 <220> FEATURE:  
47 <223> OTHER INFORMATION: Sample oligonucleotide  
E--> 48 <400> SEQUENCE: ⑤ 4 ← change to  
49 actggccgctc gttttaca 18  
50 <210> SEQ ID NO: 5  
51 <211> LENGTH: 50  
E--> 52 <212> TYPE: PNA invalid. The only <212> responses for a nucleotide sequence are: DNA or RNA  
53 <213> ORGANISM: Artificial sequence  
W--> 54 <220> FEATURE:  
55 <223> OTHER INFORMATION: Sample oligonucleotide  
W--> 56 <400> SEQUENCE: 5  
57 tgcaggcatg caagcttggc actggccgctc gttttacaac gtcgtgactg 50

*if you mean a peptide  
nucleic acid, use <212> DNA  
and explain that the  
sequence is a peptide  
nucleic acid,  
in the <2207-2223> section*

*are: DNA or  
RNA  
for a combined  
DNA/RNA  
sequence, use  
<212> DNA and  
explain in the  
<2207-2223> section*

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/601,777

DATE: 08/29/2005

TIME: 17:20:58

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\08292005\J601777.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier  
L:10 M:283 W: Missing Blank Line separator, <130> field identifier  
L:11 M:283 W: Missing Blank Line separator, <140> field identifier  
L:17 M:283 W: Missing Blank Line separator, <160> field identifier  
L:18 M:283 W: Missing Blank Line separator, <210> field identifier  
L:22 M:283 W: Missing Blank Line separator, <220> field identifier  
L:24 M:283 W: Missing Blank Line separator, <400> field identifier  
L:30 M:283 W: Missing Blank Line separator, <220> field identifier  
L:32 M:283 W: Missing Blank Line separator, <400> field identifier  
L:38 M:283 W: Missing Blank Line separator, <220> field identifier  
L:40 M:283 W: Missing Blank Line separator, <400> field identifier  
L:46 M:283 W: Missing Blank Line separator, <220> field identifier  
L:48 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:4 differs:5  
L:48 M:283 W: Missing Blank Line separator, <400> field identifier  
L:52 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:5  
L:54 M:283 W: Missing Blank Line separator, <220> field identifier  
L:56 M:283 W: Missing Blank Line separator, <400> field identifier